INPUT SET: S2805.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5        (i) APPLICANT: KIEFER, MICHAEL C.
 6                      BARR, PHILIP J.
 7
 8       (ii) TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
 9                 ENCODING THE PROTEINS AND METHODS OF USE THEREOF
10
11      (iii) NUMBER OF SEQUENCES: 22
12
13       (iv) CORRESPONDENCE ADDRESS:
14            (A) ADDRESSEE: MORRISON & FOERSTER
15            (B) STREET: 755 Page Mill Road
16            (C) CITY: Palo Alto
17            (D) STATE: California
18            (E) COUNTRY: USA
19            (F) ZIP: 94304-1018
20
21        (v) COMPUTER READABLE FORM:
22            (A) MEDIUM TYPE: Floppy disk
23            (B) COMPUTER: IBM PC compatible
24            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27       (vi) CURRENT APPLICATION DATA:
28            (A) APPLICATION NUMBER: US 08/320,157
29            (B) FILING DATE: 07-OCT-1994
30            (C) CLASSIFICATION:
31
32     (viii) ATTORNEY/AGENT INFORMATION:
33            (A) NAME: LEHNHARDT, SUSAN K.
34            (B) REGISTRATION NUMBER: 33,943
35            (C) REFERENCE/DOCKET NUMBER: 23647-20007.20
36
37       (ix) TELECOMMUNICATION INFORMATION:
38            (A) TELEPHONE: (415) 813-5600
39            (B) TELEFAX: (415) 494-0792
40            (C) TELEX: 706141
41
42
43   (2) INFORMATION FOR SEQ ID NO:1:
44
45        (i) SEQUENCE CHARACTERISTICS:
46            (A) LENGTH: 8 amino acids
```

```
47              (B) TYPE: amino acid
48              (C) STRANDEDNESS: single
49              (D) TOPOLOGY: linear
50
51            .
52
53
54
55      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
56
57       Asp Trp Gly Arg Val Val Ala Ile
58       1                 5
59
60  (2) INFORMATION FOR SEQ ID NO:2:
61
62        (i) SEQUENCE CHARACTERISTICS:
63              (A) LENGTH: 36 base pairs
64              (B) TYPE: nucleic acid
65              (C) STRANDEDNESS: single
66              (D) TOPOLOGY: linear
67
68
69
70      (ix) FEATURE:
71              (A) NAME/KEY: misc_difference
72              (B) LOCATION: replace(23, "")
73              (D) OTHER INFORMATION: /note= "This position is inosine."
74
75      (ix) FEATURE:
76              (A) NAME/KEY: misc_difference
77              (B) LOCATION: replace(27, "")
78              (D) OTHER INFORMATION: /note= "This position is inosine."
79
80
81      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
82
83  AGATCTGAAT TCAACTTGGG GGNCAGNAGT NGTNGC                                    36
84
85  (2) INFORMATION FOR SEQ ID NO:3:
86
87        (i) SEQUENCE CHARACTERISTICS:
88              (A) LENGTH: 11 amino acids
89              (B) TYPE: amino acid
90              (C) STRANDEDNESS: single
91              (D) TOPOLOGY: linear
92
93
94
95
96
97      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
98
99       Asp Trp Gly Gly Gln Glu Asn Asp Gln Ile Trp
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100        1              5              10
101
102    (2) INFORMATION FOR SEQ ID NO:4:
103
104        (i) SEQUENCE CHARACTERISTICS:
105             (A) LENGTH: 29 base pairs
106             (B) TYPE: nucleic acid
107             (C) STRANDEDNESS: single
108             (D) TOPOLOGY: linear
109
110
111
112        (ix) FEATURE:
113             (A) NAME/KEY: misc_difference
114             (B) LOCATION: replace(6, "")
115             (D) OTHER INFORMATION: /note= "This position is inosine."
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117        (ix) FEATURE:
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119             (B) LOCATION: replace(9, "")
120             (D) OTHER INFORMATION: /note= "This position is inosine."
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122
123        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
124
125    AGGGTNGGNG GNACNAGAGA CATCTAGGT                                29
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127    (2) INFORMATION FOR SEQ ID NO:5:
128
129        (i) SEQUENCE CHARACTERISTICS:
130             (A) LENGTH: 41 base pairs
131             (B) TYPE: nucleic acid
132             (C) STRANDEDNESS: single
133             (D) TOPOLOGY: linear
134
135
136
137        (ix) FEATURE:
138             (A) NAME/KEY: misc_difference
139             (B) LOCATION: replace(19, "")
140             (D) OTHER INFORMATION: /note= "This position is inosine."
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142        (ix) FEATURE:
143             (A) NAME/KEY: misc_difference
144             (B) LOCATION: replace(22, "")
145             (D) OTHER INFORMATION: /note= "This position is inosine."
146
147
148        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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150    AGATCTAAGC TTGTCCCANC CNCCNTGNTC CTTGAGATCC A                  41
151
152    (2) INFORMATION FOR SEQ ID NO:6:
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INPUT SET: S2805.raw

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154          (i) SEQUENCE CHARACTERISTICS:
155               (A) LENGTH: 2094 base pairs
156               (B) TYPE: nucleic acid
157               (C) STRANDEDNESS: single
158               (D) TOPOLOGY: linear
159
160
161
162          (ix) FEATURE:
163               (A) NAME/KEY: CDS
164               (B) LOCATION: 201..833
165
166
167          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
168
169    GAGGATCTAC AGGGGACAAG TAAAGGCTAC ATCCAGATGC CGGGAATGCA CTGACGCCCA      60
170
171    TTCCTGGAAA CTGGGCTCCC ACTCAGCCCC TGGGAGCAGC AGCCGCCAGC CCCTCGGACC     120
172
173    TCCATCTCCA CCCTGCTGAG CCACCCGGGT TGGGCCAGGA TCCCGGCAGG CTGATCCCGT     180
174
175    CCTCCACTGA GACCTGAAAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC        230
176                          Met Ala Ser Gly Gln Gly Pro Gly Pro Pro
177                           1               5                  10
178
179    AGG CAG GAG TGC GGA GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG     278
180    Arg Gln Glu Cys Gly Glu Pro Ala Leu Pro Ser Ala Ser Glu Glu Gln
181                15                  20                  25
182
183    GTA GCC CAG GAC ACA GAG GAG GTT TTC CGC AGC TAC GTT TTT TAC CGC     326
184    Val Ala Gln Asp Thr Glu Glu Val Phe Arg Ser Tyr Val Phe Tyr Arg
185                30                  35                  40
186
187    CAT CAG CAG GAA CAG GAG GCT GAA GGG GTG GCT GCC CCT GCC GAC CCA     374
188    His Gln Gln Glu Gln Glu Ala Glu Gly Val Ala Ala Pro Ala Asp Pro
189                45                  50                  55
190
191    GAG ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG     422
192    Glu Met Val Thr Leu Pro Leu Gln Pro Ser Ser Thr Met Gly Gln Val
193                60                  65                  70
194
195    GGA CGG CAG CTC GCC ATC ATC GGG GAC GAC ATC AAC CGA CGC TAT GAC     470
196    Gly Arg Gln Leu Ala Ile Ile Gly Asp Asp Ile Asn Arg Arg Tyr Asp
197    75                  80                  85                  90
198
199    TCA GAG TTC CAG ACC ATG TTG CAG CAC CTG CAG CCC ACG GCA GAG AAT     518
200    Ser Glu Phe Gln Thr Met Leu Gln His Leu Gln Pro Thr Ala Glu Asn
201                    95                  100                 105
202
203    GCC TAT GAG TAC TTC ACC AAG ATT GCC ACC AGC CTG TTT GAG AGT GGC     566
204    Ala Tyr Glu Tyr Phe Thr Lys Ile Ala Thr Ser Leu Phe Glu Ser Gly
205                    110                 115                 120
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INPUT SET: S2805.raw

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206
207   ATC AAT TGG GGC CGT GTG GTG GCT CTT CTG GGC TTC GGC TAC CGT CTG      614
208   Ile Asn Trp Gly Arg Val Val Ala Leu Leu Gly Phe Gly Tyr Arg Leu
209           125                   130                   135
210
211   GCC CTA CAC GTC TAC CAG CAT GGC CTG ACT GGC TTC CTA GGC CAG GTG      662
212   Ala Leu His Val Tyr Gln His Gly Leu Thr Gly Phe Leu Gly Gln Val
213           140                   145                   150
214
215   ACC CGC TTC GTG GTC GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG      710
216   Thr Arg Phe Val Val Asp Phe Met Leu His His Cys Ile Ala Arg Trp
217   155                   160                   165                   170
218
219   ATT GCA CAG AGG GGT GGC TGG GTG GCA GCC CTG AAC TTG GGC AAT GGT      758
220   Ile Ala Gln Arg Gly Gly Trp Val Ala Ala Leu Asn Leu Gly Asn Gly
221                   175                   180                   185
222
223   CCC ATC CTG AAC GTG CTG GTG GTT CTG GGT GTG GTT CTG TTG GGC CAG      806
224   Pro Ile Leu Asn Val Leu Val Val Leu Gly Val Val Leu Leu Gly Gln
225                   190                   195                   200
226
227   TTT GTG GTA CGA AGA TTC TTC AAA TCA TGACTCCCAA GGGTGCCCTT          853
228   Phe Val Val Arg Arg Phe Phe Lys Ser
229                   205                   210
230
231   TGGGTCCCGG TTCAGACCCC TGCCTGGACT TAAGCGAAGT CTTTGCCTTC TCTGTTCCCT   913
232
233   TGCAGGGTCC CCCCTCAAGA GTACAGAAGC TTTAGCAAGT GTGCACTCCA GCTTCGGAGG   973
234
235   CCCTGCGTGG GGGCCAGTCA GGCTGCAGAG GCACCTCAAC ATTGCATGGT GCTAGTGCCC   1033
236
237   TCTCTCTGGG CCCAGGGCTG TGGCCGTCTC CTCCCTCAGC TCTCTGGGAC CTCCTTAGCC   1093
238
239   CTGTCTGCTA GGCGCTGGGG AGACTGATAA CTTGGGGAGG CAAGAGACTG GGAGCCACTT   1153
240
241   CTCCCCAGAA AGTGTTTAAC GGTTTTAGCT TTTTATAATA CCCTTGTGAG AGCCCATTCC   1213
242
243   CACCATTCTA CCTGAGGCCA GGACGTCTGG GGTGTGGGGA TTGGTGGGTC TATGTTCCCC   1273
244
245   AGGATTCAGC TATTCTGGAA GATCAGCACC CTAAGAGATG GGACTAGGAC CTGAGCCTGG   1333
246
247   TCCTGGCCGT CCCTAAGCAT GTGTCCCAGG AGCAGGACCT ACTAGGAGAG GGGGGCCAAG   1393
248
249   GTCCTGCTCA ACTCTACCCC TGCTCCCATT CCTCCCTCCG GCCATACTGC CTTTGCAGTT   1453
250
251   GGACTCTCAG GGATTCTGGG CTTGGGGTGT GGGGTGGGGT GGAGTCGCAG ACCAGAGCTG   1513
252
253   TCTGAACTCA CGTGTCAGAA GCCTCCAAGC CTGCCTCCCA AGGTCCTCTC AGTTCTCTCC   1573
254
255   CTTCCTCTCT CCTTATAGAC ACTTGCTCCC AACCCATTCA CTACAGGTGA AGGCTCTCAC   1633
256
257   CCATCCCTGG GGGCCTTGGG TGAGTGGCCT GCTAAGGCTC CTCCTTGCCC AGACTACAGG   1693
258
```

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☑ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7. Other: ————————————————————————————————

Applicant must provide:

☑ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

☑ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☑ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

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